

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/719,272

DATE: 02/05/2001

TIME: 16:33:48

Input Set : A:\36959sequence.txt

Output Set: N:\CRF3\02052001\I719272.raw

#6
py
6.8.01

4 <110> APPLICANT: YAMAMOTO, Hiroshi
 5 TSUJIKAWA, Kazutake
 6 UCHINO, Yukiko
 7 KONISHI, Noboru
 9 <120> TITLE OF INVENTION: ANTIRODIES SPECIFIC FOR PHOSPHATASE SUBUNIT FOR LAR
 11 <130> FILE REFERENCE: 19036/36959
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/719,272
 C--> 14 <141> CURRENT FILING DATE: 2000-12-08
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP98/02542
 17 <151> PRIOR FILING DATE: 1998-06-08
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/03054
 20 <151> PRIOR FILING DATE: 1999-06-07
 22 <160> NUMBER OF SEQ ID NOS: 3
 24 <170> SOFTWARE: PatentIn Ver. 2.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3467
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (6)..(1826)
 35 <220> FEATURE:
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 37 <222> LOCATION: (213)..(953)
 38 <223> OTHER INFORMATION: Phosphate Domain 1
 40 <220> FEATURE:
 41 <221> NAME/KEY: misc_feature
 42 <222> LOCATION: (1080)..(1826)
 43 <223> OTHER INFORMATION: Phosphate Domain 2
 45 <300> PUBLICATION INFORMATION:
 46 <308> DATABASE ACCESSION NO: DDBJ/EMBL/GenBank Accession No. Y00815
 47 <309> DATABASE ENTRY DATE: 1995-09-19
 49 <400> SEQUENCE: 1
 50 gatcc gga ctg aag gac tcc ttg ctg gcc cac tcc tct gac cct gtg gag 50
 51 Gly Leu Lys Asp Ser Leu Leu Ala His Ser Asp Pro Val Glu
 52 1 5 10 15
 56 atg cgg agg ctc aac tac cag acc cca ggt atg cga gac cac cca ccc 98
 57 Met Arg Arg Leu Asn Tyr Gln Thr Pro Gly Met Arg Asp His Pro Pro
 58 20 25 30
 60 atc ccc atc acc gac ctg gcg gac aac atc gag cgc ctc aaa gcc aac 146
 61 Ile Pro Ile Thr Asp Leu Ala Asp Asn Ile Glu Arg Leu Lys Ala Asn
 62 35 40 45
 64 gat ggc ctc aag ttc tcc cag gag tat gag tcc atc gac cct gga cag 194
 65 Asp Gly Leu Lys Phe Ser Gln Glu Tyr Glu Ser Ile Asp Pro Gly Gln
 66 50 55 60
 68 cag ttc acg tgg gag aat tca aac ctg gag gtg aac aag ccc aag aac 242
 69 Gln Phe Thr Trp Glu Asn Ser Asn Leu Glu Val Asn Lys Pro Lys Asn

ENTERED

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70      65      70      75
72 cgc tat gcg aat gtc atc gcc tac gac cac tct cga gtc atc ctt acc 290
73 Arg Tyr Ala Asn Val Ile Ala Tyr Asp His Ser Arg Val Ile Leu Thr
74 80      85      90      95
76 tct atc gat ggc gtc ccc ggg agt gac tac atc aat gcc aac tac atc 338
77 Ser Ile Asp Gly Val Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile
78      100      105      110
80 gat ggc tac cgc aag cag aat gcc tac atc gcc acg cag ggc ccc ctg 386
81 Asp Gly Tyr Arg Lys Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu
82      115      120      125
84 ccc gag acc atg ggc gat ttc tgg aga atg gtg tgg gaa cag cgc acg 434
85 Pro Glu Thr Met Gly Asp Phe Trp Arg Met Val Trp Glu Gln Arg Thr
86      130      135      140
88 gcc act gtg gtc atg atg aca cgg ctg gag gag aag tcc cgc gta aaa 482
89 Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys Ser Arg Val Lys
90      145      150      155
92 tgt gat cag tac tgg cca gcc cgt ggc acc gag acc tgt ggc ctt att 530
93 Cys Asp Gln Tyr Trp Pro Ala Arg Gly Thr Glu Thr Cys Gly Leu Ile
94 160      165      170      175
96 cag gtg acc ctg ttg gac aca gtg gag ctg gcc aca tac act gtg cgc 578
97 Gln Val Thr Leu Leu Asp Thr Val Glu Leu Ala Thr Tyr Thr Val Arg
98      180      185      190
100 acc ttc gca ctc cac aag agt ggc tcc agt gag aag cgt gag ctg cgt 626
101 Thr Phe Ala Leu His Lys Ser Gly Ser Ser Glu Lys Arg Glu Leu Arg
102      195      200      205
104 cag ttt cag ttc atg gcc tgg cca gac cat gga gtt cct gag tac cca 674
105 Gln Phe Gln Phe Met Ala Trp Pro Asp His Gly Val Pro Glu Tyr Pro
106      210      215      220
108 act ccc atc ctg gcc ttc cta cga cgg gtc aag gcc tgc aac ccc cta 722
109 Thr Pro Ile Leu Ala Phe Leu Arg Arg Val Lys Ala Cys Asn Pro Leu
110      225      230      235
112 gac gca ggg ccc atg gtg gtg cac tgc agc gcg ggc gtg ggc cgc acc 770
113 Asp Ala Gly Pro Met Val Val His Cys Ser Ala Gly Val Gly Arg Thr
114 240      245      250      255
116 ggc tgc ttc atc gtg att gat gcc atg ttg gag cgg atg aag cac gag 818
117 Gly Cys Phe Ile Val Ile Asp Ala Met Leu Glu Arg Met Lys His Glu
118      260      265      270
120 aag acg gtg gac atc tat gcc cac gtg acc tgc atg cga tca cag agg 866
121 Lys Thr Val Asp Ile Tyr Gly His Val Thr Cys Met Arg Ser Gln Arg
122      275      280      285
124 aac tac atg gtg cag acg gag gac cag tac gtg ttc atc cat gag gcg 914
125 Asn Tyr Met Val Gln Thr Glu Asp Gln Tyr Val Phe Ile His Glu Ala
126      290      295      300
128 ctg ctg gag gct gcc acg tgc ggc cac aca gag gtg cct gcc cgc aac 962
129 Leu Leu Glu Ala Ala Thr Cys Gly His Thr Glu Val Pro Ala Arg Asn
130      305      310      315
132 ctg tat gcc cac atc cag aag ctg ggc caa gtg cct cca ggg gag agt 1010
133 Leu Tyr Ala His Ile Gln Lys Leu Gly Gln Val Pro Pro Gly Glu Ser
134 320      325      330      335

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136 gtg acc gcc atg gag ctc gag ttc aag ttg ctg gcc agc tcc aag gcc 1058
137 Val Thr Ala Met Glu Leu Glu Phe Lys Leu Leu Ala Ser Ser Lys Ala
138 340 345 350
140 cac acg tcc cgc ttc atc agc gcc aac ctg ccc tgc aac aag ttc aag
141 His Thr Ser Arg Phe Ile Ser Ala Asn Leu Pro Cys Asn Lys Phe Lys 1106
142 355 360 365
144 aac cgg ctg gtg aac atc atg ccc tac gaa ttg acc cgt gtg tgt ctg
145 Asn Arg Leu Val Asn Ile Met Pro Tyr Glu Leu Thr Arg Val Cys Leu 1154
146 370 375 380
148 cag ccc atc cgt ggt gtg gag ggc tct gac tac atc aat gcc agc ttc
149 Gln Pro Ile Arg Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe 1202
150 385 390 395
152 ctg gat ggt tat aga cag cag aag gcc tac ata gct aca cag ggg cct
153 Leu Asp Gly Tyr Arg Gln Gln Lys Ala Tyr Ile Ala Thr Gln Gly Pro 1250
154 400 405 410 415
156 ctg gca gag agc acc gag gac ttc tgg cgc atg cta tgg gag cac aat
157 Leu Ala Glu Ser Thr Glu Asp Phe Trp Arg Met Leu Trp Glu His Asn 1298
158 420 425 430
160 tcc acc atc atc gtc atg ctg acc aag ctt cgg gag atg ggc agg gag
161 Ser Thr Ile Ile Val Met Leu Thr Lys Leu Arg Glu Met Gly Arg Glu 1346
162 435 440 445
164 aaa tgc cac cag tac tgg cca gca gag cgc tct gct cgc tac cag tac
165 Lys Cys His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr 1394
166 450 455 460
168 ttt gtt gtt gac ccg atg gct gag tac aac atg ccc cag tat atc ctg
169 Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Glu Tyr Ile Leu 1442
170 465 470 475
172 cgt gag ttc aag gtc acg gat gcc cgg gat ggg cag tca agg aca atc
173 Arg Glu Phe Lys Val Thr Asp Ala Arg Asp Gly Gln Ser Arg Thr Ile 1490
174 480 485 490 495
176 cgg cag ttc cag ttc aca gac tgg cca gag cag ggc gtg ccc aag aca
177 Arg Gln Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Val Pro Lys Thr 1538
178 500 505 510
180 ggc gag gga ttc att gac ttc atc ggg cag gtg cat aag acc aag gag
181 Gly Glu Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys Glu 1586
182 515 520 525
184 cag ttt gga cag gat ggg cct atc acg gtg cac tgc agt gct ggc gtg
185 Gln Phe Gly Gln Asp Gly Pro Ile Thr Val His Cys Ser Ala Gly Val 1634
186 530 535 540
188 ggc cgc acc ggg gtg ttc atc act ctg agc atc gtc ctg gag cgc atg
189 Gly Arg Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg Met 1682
190 545 550 555
192 cgc tat gag ggc gtg gtc gac atg ttt cag acc gtg aag acc ctg cgt
193 Arg Tyr Glu Gly Val Val Asp Met Phe Gln Thr Val Lys Thr Leu Arg 1730
194 560 565 570 575
196 aca cag cgt cct gcc atg gtg cag aca gag gac cag tat cag ctg tgc
197 Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Gln Tyr Gln Leu Cys 1778
198 580 585 590
200 tac cgt gcg gcc ctg gag tac ctc ggc agc ttt gac cac tat gca acg 1826

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201 Tyr Arg Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr
202      595      600      605
204 taactaccgc tcccctctcc tccqccaccc ccgccgtggg qctccggagg ggacccagct 1886
206 cctctgagcc ataccgacca tcgtccagcc ctctacgca gatgctgtca ctggcagagc 1946
208 acagcccacg gggatcacag cgtttcagga acgttgccac accaatcaga gagcctagaa 2006
210 catccctggg caagtggatg gccacgacag caggcactgt ggcccttctg tccaccagac 2066
212 ccacctggag cccgcttcaa gctctctgtt gcgctcccgc atttctcatg cttcttctca 2126
214 tgggggtggg ttggggcaaa gcctcctttt taatacatra agtggggtag actgagggat 2186
216 tttagcctct tccctctgat ttttctttt gcgaatccgt atctgcagaa tgggccactg 2246
218 taggggttgg gggtttattt gttttgtttt tttttttttt ttgtatgact tctgctgaag 2306
220 gacagaacat tgccttcttc gtgcagagct ggggctgcca gcctgagcgg aggctcggcc 2366
222 gtgggcccgg aggcagtgtt gatccggctg ctctccagc ccttcagacg agatcctgtt 2426
224 tcaqctaaat gcagggaaac tcaatgtttt ttttaagttt gttttccctt taaagccttt 2486
226 ttttaggcca cattgacagt ggtgggcccgg gagaagatag ggaacactca tccctggctg 2546
228 tctatcccag tgtgtgttta acattcacag ccagaaacca cagatgtgtc tgggagagcc 2606
230 tggcaaggca ttctctatca ccatcgtgtt tgcgaagggt aaaaacaaaa caaaaaacca 2666
232 caaaaaataa aacaaaaaaa ccaaaaaaac ccaaaaaaaa aaaaaaaaag agtcagccct 2726
234 tggtctctgc tcaaaaccct caagagggga agcaactccg tgtgcctggg gttcccagg 2786
236 gagctgctgg ctgacctggg cccacagagc ctggcttttg tcccagcat tgcagtatgg 2846
238 tgtggtgttt gtaqgctgtg gggctctggc gtgtggccaa ggtgaatagc acaggttagg 2906
240 gtgtgtgcca caccctatgc acctcagggc caagcggggg cgtggctggc ctttcaggtc 2966
242 caggccagtg ggcctggtag cacatgtctg tcttcagagc aggggccaga tgattttcct 3026
244 ccttgggttg cagctgtttt caaagcccc gataatcgct cttttccact ccaagatgcc 3086
246 ctcataaacc aatgtggcaa gactactgga cttctatcaa tggtaactta atcagtcctt 3146
248 attatcccag ctgtctgagg ggcagggaga gcgcctcttc ctctgggagc cgctatctag 3206
250 ataggtaagt gggggcgggg aagggtgcat agctgtttta gctgagggac gtggtgccga 3266
252 cgtcccaaaa cctagctagg ctaagtcaag atcaacatlc cagggttggg aatgttggat 3326
254 gatgaaacat tcatttttac cttgtggatg ctagtgtctt agagtccact gttgtacaca 3386
256 gtctgttttc tatttgttaa gaaaaactac agcatcattg cataattcct gatggtaata 3446
258 aatttgaata atcagatttc t                                     3467
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262 <211> LENGTH: 11
263 <212> TYPE: PRT
264 <213> ORGANISM: Unknown
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Unknown Organism: Signature Motif
268 Conserved in Phosphatase Domain of Known PTPs.
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271 <221> NAME/KEY: SITE
272 <222> LOCATION: (1)
273 <223> OTHER INFORMATION: Xaa= Ile or Val
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276 <221> NAME/KEY: SITE
277 <222> LOCATION: (4)
278 <223> OTHER INFORMATION: Xaa=Unknown
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282 <222> LOCATION: (7)..(8)
283 <223> OTHER INFORMATION: Xaa=Unknown

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287 <222> LOCATION: (10)
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304 <220> FEATURE:
305 <221> NAME/KEY: sig_peptide
306 <222> LOCATION: (371)..(418)
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309 <221> NAME/KEY: mat_peptide
310 <222> LOCATION: (419)..(6061)
312 <220> FEATURE:
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315 <223> OTHER INFORMATION: Extracellular Domain
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320 <223> OTHER INFORMATION: Transmembrane Domain
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324 <222> LOCATION: (4193)..(6061)
325 <223> OTHER INFORMATION: Cytoplasmic Domain
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336 cgggaccagg tggaggcggc ggcggcagag gagtgggagc agcggcccta gcgcttgcg 180
338 gggggacatg cggaccgacg gccctggat aggcggaagg agtggaggcc ctggtgcccg 240
340 gcccttgggt ctgagtatcc agcaagagtg accgggggtga agaagcaaag actcgggtga 300
342 ttgtcctggg ctgtggctgg ctgtggagct agagccctgg atggccctg agccagcccc 360
344 agggaggagc atg gtg ccc ctt gtg cct gca ctg gtg atg ctt ggt ttg 409
345      Met Val Pro Leu Val Pro Ala Leu Val Met Leu Gly Leu
346      -15                      -10                      -5
348 gtg gca ggc gcc cat ggt gac agc aaa cct gtc ttc att aaa gtc cct 457
349 Val Ala Gly Ala His Gly Asp Ser Lys Pro Val Phe Ile Lys Val Pro
350      -1   1           5           10
352 gag gac cag act ggg ctg tca gga ggg gta gcc tcc ttc gtg tgc caa 505

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L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:291 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2